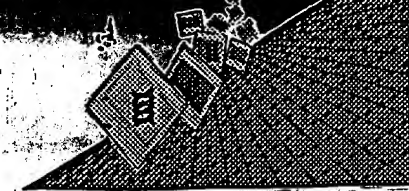


# RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/992,238

Source: OIP

Date Processed by STIC: 12/3/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

## Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

## Raw Sequence Listing Error Summary

### ERROR DETECTED      SUGGESTED CORRECTION

SERIAL NUMBER: 09/992,238

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file  
     Wrapped Aminos      was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will  
                                  prevent "wrapping."
  
- 2      Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
  
- 3      Misaligned Amino      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers;  
     Numbering                  use space characters, instead.
  
- 4      Non-ASCII              The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please  
                                  ensure your subsequent submission is saved in ASCII text.
  
- 5      Variable Length      Sequence(s)          contain n's or Xaa's representing more than one residue. Per Sequence Rules,  
                                  each n or Xaa can only represent a single residue. Please present the maximum number of each  
                                  residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6      PatentIn 2.0      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
     "bug"                      sequences(s)         . Normally, PatentIn would automatically generate this section from the  
                                  previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to  
                                  the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for  
                                  Artificial or Unknown sequences.
  
- 7      Skipped Sequences      Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence:  
     (OLD RULES)              (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                  (i)      SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                                  (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                  This sequence is intentionally skipped  
  
                                  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
  
- 8      Skipped Sequences      Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence.  
     (NEW RULES)              <210> sequence id number  
                                  <400> sequence id number  
                                  000
  
- 9   ✓   Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
     (NEW RULES)              Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                                  In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 10      Invalid <213>      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or  
     Response                  scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or  
                                  is Artificial Sequence
  
- 11      Use of <220>      Sequence(s)          missing the <220> "Feature" and associated numeric identifiers and responses.  
                                  Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or  
                                  "Unknown." Please explain source of genetic material in <220> to <223> section.  
                                  (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12      PatentIn 2.0      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,  
     "bug"                      resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence  
                                  listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/992,238

DATE: 12/03/2001  
 TIME: 14:27:50

Input Set : A:\D0047.ST25.txt  
 Output Set: N:\CRF3\11212001\I992238.raw

**Does Not Comply  
 Corrected Diskette Needed**

*Errors on pp. 1, 3, 5*

3 <110> APPLICANT: BATTAGLINO, PETER  
 4 FEDER, JOHN N  
 5 MINTIER, GABE  
 6 NELSON, THOMAS C  
 7 RAMANATHAN, CHANDRA S  
 8 WESTPHAL, RYAN  
 9 CACACE, ANGELA  
 10 BARBER, LAUREN  
 11 HAWKEN, DONALD R  
 12 KORNACKER, MICHAEL G  
 14 <120> TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY8,  
 15 EXPRESSED HIGHLY IN BRAIN  
 17 <130> FILE REFERENCE: D0047NP  
 C--> 19 <140> CURRENT APPLICATION NUMBER: US/09/992,238  
 C--> 20 <141> CURRENT FILING DATE: 2001-11-14  
 22 <150> PRIOR APPLICATION NUMBER: 60/317166  
 23 <151> PRIOR FILING DATE: 2001-09-04  
 25 <150> PRIOR APPLICATION NUMBER: 60/308285  
 26 <151> PRIOR FILING DATE: 2001-07-27  
 28 <150> PRIOR APPLICATION NUMBER: 60/268581  
 29 <151> PRIOR FILING DATE: 2001-02-14  
 31 <150> PRIOR APPLICATION NUMBER: 60/248285  
 32 <151> PRIOR FILING DATE: 2000-11-14  
 34 <160> NUMBER OF SEQ ID NOS: 102  
 36 <170> SOFTWARE: PatentIn Ver. 2.1

#### ERRORED SEQUENCES

3624 <210> SEQ ID NO: 102  
 3625 <211> LENGTH: 21  
 3626 <212> TYPE: PRT  
 3627 <213> ORGANISM: Artificial Sequence  
 3629 <220> FEATURE:  
 3630 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 3631 polypeptide  
 3633 <400> SEQUENCE: 102  
 3634 Ser Val Val Ser Phe Ile Val Ile Pro Leu Ile Val Met Ile Ala Cys  
 3635 1 5 10 15  
 3637 Tyr Ser Val Val Phe  
 3638 20  
 E--> 3643 D0047 NP  
 E--> 3647 - 1 - - delete

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/992,238

DATE: 12/03/2001

TIME: 14:27:52

Input Set : A:\D0047.ST25.txt

Output Set: N:\CRF3\11212001\I992238.raw

L:19 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:20 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:2795 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:48  
L:2795 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:48  
L:2795 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48  
L:2806 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:48  
L:2806 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:48  
L:2806 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48  
L:2808 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:48  
L:2808 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:48  
L:2808 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48  
L:2847 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:49  
L:2847 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:49  
L:2847 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49  
L:2889 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:49  
L:2889 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:49  
L:2889 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49  
L:2898 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:49  
L:2898 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:49  
L:2898 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49  
L:3092 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:63  
L:3092 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:63  
L:3092 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63  
L:3093 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:63  
L:3093 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:63  
L:3093 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63  
L:3106 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:64  
L:3106 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:64  
L:3106 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64  
L:3107 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:64  
L:3107 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:64  
L:3107 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64  
L:3643 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:3643 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2  
L:3647 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:102  
L:3647 M:252 E: No. of Seq. differs, <211>LENGTH:Input:21 Found:23 SEQ:102

<210> 48  
<211> 1527  
<212> DNA  
<213> Homo sapiens

<220>  
<223> N=A+T+G+C

→ must give location of n  
- see error summary sheet, item 9

<400> 48

atgacgtcca cctgcaccaa cagcacgcgc gagagtaaca gcagccacac gtgcatgcc 60  
ctctccaaaa tgcccatcag cctggccac gccatcatcc gctcaaccgt gctggttatc 120

<210> 49  
<211> 508  
<212> PRT  
<213> Homo sapiens

*Some error for Xaa*

<220>  
<223> Xaa=Unknown, modified, or any amino acid

<400> 49

Met	Thr	Ser	Thr	Cys	Thr	Asn	Ser	Thr	Arg	Glu	Ser	Asn	Ser	Ser	His
1				5					10					15	

Thr Cys Met Pro Leu Ser Lys Met Pro Ile Ser Leu Ala His Gly Ile

<210> 63

<211> 99

<212> DNA

<213> Artificial Sequence

*Some error*

<220>

<223> Description of Artificial Sequence: Oligo 1;

N=A+G+C+T and B=C+G+T

<400> 63

cgaagcgtaa gggcccagcc ggccnnbnnb nnbnnbnnbn nbnnbnnbnn bnnbnnbnnb 60  
nnbnnbnnbn nbnnbnnbnn bnnbccgggt ccgggcggc 99

<210> 64

<211> 95

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo 2;

N=A+G+C+T and V=C+A+G

<400> 64

aaaaggaaaa aagcggccgc vnnvnnvnnv nnvnnvnnvn nvnnvnnvnn vnnvnnvnnv 60  
nnvnnvnnvn nvnnvnnvnn gccgcccgga cccgg 95